

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/561,504
Source: IFWP
Date Processed by STIC: 12/29/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/561,504

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW

RAW SEQUENCE LISTING

DATE: 12/29/2005

PATENT APPLICATION: US/10/561,504

TIME: 15:04:31

Input Set : A:\304561_Sequence_Listing.txt

Output Set: N:\CRF4\12292005\J561504.raw

3 <110> APPLICANT: Tamai, Ikumi
 4 Nozawa, Takashi
 6 <120> TITLE OF INVENTION: Screening Method for Therapeutic Agent for Breast Cancer
 8 <130> FILE REFERENCE: 051009/304561
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/561,504
 C--> 11 <141> CURRENT FILING DATE: 2005-12-19
 13 <160> NUMBER OF SEQ ID NOS: 22
 15 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

**Does Not Comply
 Corrected Diskette Needed**

269 <210> SEQ ID NO: 22
 270 <211> LENGTH: 20
 271 <212> TYPE: DNA
 272 <213> ORGANISM: Artificial
 274 <220> FEATURE:
 275 <223> OTHER INFORMATION: AT4
 277 <400> SEQUENCE: 22
 278 gagattggaa cccagtctct

E--> 282 5
 E--> 285 5
 E--> 287 rta01/2195262v1
 E--> 289 rta01/2195262v1

*delete
 at end of file*

*insufficient explanation
 (give source of genetic material)
 20
 (see item 11
 on Error summary sheet)*

see p. 2

10/561,504 2

SEQUENCE LISTING

<110> Tamai, Ikumi
Nozawa, Takashi

<120> Screening Method for Therapeutic Agent for Breast Cancer

<130> 051009/304561

<140> JP2003-177021
<141> 2003-06-20

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 20

<212> DNA

<213> Artificial

<220>

<223> ATP-A

<400> 1

aaacaagctg cccacatagg

*another example of an insufficient explanation
for <213> Artificial*

(global error)

20

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 12/29/2005

PATENT APPLICATION: US/10/561,504

TIME: 15:04:32

Input Set : A:\304561_Sequence_Listing.txt

Output Set: N:\CRF4\12292005\J561504.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:282 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:285 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:25 SEQ:22
L:287 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:287 M:112 C: (48) String data converted to lower case,
L:289 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:30 SEQ:22
L:289 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:289 M:112 C: (48) String data converted to lower case,
L:289 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:30 SEQ:22